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Chromosomal Organization by an Interplay of Loop Extrusion and Compartment Interaction¹ JOHANNES NUEBLER, GEOFFREY FUNDENBERG, MAXIM IMAKAEV, CAROLYN LU, ANTON GOLOBORODKO, NEZAR ABDENNUR, LEONID MIRNY, Institute for Medical Engineering and Science, Massachusetts Institute of Technology (MIT), Cambridge, MA 02139, USA — The chromatin fiber in eukaryotic nuclei is far from being simply a confined but otherwise randomly arranged polymer. Rather, it shows a high degree of spatial organization on all length scales, from individual nucleosomes up to well-segregated chromosome territories. On intermediate scales, chromosome conformation capture techniques have revealed two ubiquitous modes of organization: an alternating structure of A/B compartments, where each type preferentially associates with other base pairs of its type, and, typically on a smaller scale, the formation of topologically associating domains (TADs) with increased association within each domain but not across boundaries. The mechanisms behind this organization are only beginning to emerge. We review how the model of active loop extrusion can explain in a unified way such diverse phenomena as TAD formation and mitotic compaction and segregation, and we address in particular to what extent the interplay of active loop extrusion and compartment structure is compatible with recent experiments that interfere with the loading of the proposed loop extrusion factor cohesin.

¹4D Nucleome

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